

10/643,589
Sequence alignment B
US-08-633-148-2
; Sequence 2, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSER, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-005600US
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-2

Query Match 84.6%; Score 1807; DB 1; Length 340;
Best Local Similarity 99.7%; Pred. No. 4.3e-138;
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAAGTAVGAWVLVLSLWGAVVGAQNITARIGEPLVLKCKGAKPKPPQRLEWKLNTRTEA 60
Db 1 MAAGTAVGAWVLVLSLWGAVVGAQNITARIGEPLVLKCKGAKPKPPQRLEWKLNTRTEA 60

Qy 61 WKVLSPQGGGPWDSVARVLPGNGSLFLPAVGIQDEGIFRCQAMNRNGKETHSNYRVRYQI 120
Db 61 WKVLSPQGGGPWDSVARVLPGNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120

Qy 121 PGKPEIVDSASELTAGVPNKGTCVSEGSYPAGTLSWHLGKPLVPNEKGVSVKEQTRRH 180
Db 121 PGKPEIVDSASELTAGVPNKGTCVSEGSYPAGTLSWHLGKPLVPNEKGVSVKEQTRRH 180

Qy 181 PETGLFTLQSELMTPARGGDPRPTFSCSFSPGLPRHRLRTAPIQPRVWEPPVLEEVQL 240
Db 181 PETGLFTLQSELMTPARGGDPRPTFSCSFSPGLPRHRLRTAPIQPRVWEPPVLEEVQL 240

Qy 241 VVEPEGGAVAPGGTVILTCEVPAQPSPOIHWMKDGVPLPLPPSPVILPEIGPQDQGTYS 300
Db 241 VVEPEGGAVAPGGTVILTCEVPAQPSPOIHWMKDGVPLPLPPSPVILPEIGPQDQGTYS 300

Qy 301 CVATHSSHPQESRAVSISIIEPGEEGPTAGSVGGSGLGT 340
Db 301 CVATHSSHPQESRAVSISIIEPGEEGPTAGSVGGSGLGT 340